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TCAAGACGA GTTATTTTCA GCTGCTgaCT GGAGACGGTG CAGCTCTGGA TACGAGAGCA TTTCCTACTAT GGGACTGGAT ACAACACAC ACCGGGAGA CTTCAAGAGT TTCAGACTGA
 GGAGAAAC TTTCCCTTCT GCTGCTACTG CTGCTGCCG TCGTTTGA AGTCCTCTC TTTCATGTT TTTTCTGCT CACCTTCGCT GCTGCCGCTG TTCTCTTTGG
 TTCTATTGAG CGGCTGGCCA GAGGATGAGA CTTCCCAAC TCTCCTTTT TACCTGCTT GCTGAGCTT GGAATTCATC TGCACTGTGT TGGGTGCCCC TGACTTGGCC 32
 M R L P K L L T F L L W Y L A W L D L E F I C T V L G A P D L G
 CAGAGACCC AGGGTTCAG GCCAGGATTG GCCAAGCAG AGGCCCCCG GAGGCCCGG AGCTCTTCAG GCCAGGGGT CACAGCTATG GTGGGGGGC CACCAATGCC 72
 Q R P Q G S R P G L A K A E A K E R P P L A R N V F R P G G H S Y G G A T N A
 ATGCTGAGG CACGGGAGG CACGGGAGG ACAGGAGCC TGACACAGCC CAGNAGGAT GAACCAAAA AGCTGCCCC CAGACCGGG GGCCTGAAC CCAAGCCAGG ACACCTGCC
 N A R A K G G T G Q T G G L T Q P K K D E P K K L P P R P G G P E P K P G H P P 112
 CAAACAGCC AGCTACAGC CCGACTGTG ACCCCAAAG GACAGCTTCC CGGAGGCAAG GCACCCCAA AAGCAGATC TGTCCCCAG TCTTCTGCTG TGAAGAGGC CAGGAGGCC
 Q T R Q A T A R T V T P K G Q L P G K A P P K A G S V P S S F L L K A R E P 152
 GGGCCCCAC GAGAGCCAA GGAGCGTTT CCGCCACCC CCATCACACC CCAGAGTAC ATGCTCTGCTG TGTACAGAC GCTGTCCGAT GCTGACAGAA AGGAGGCAA CAGCAGCGTG
 G P P R E P K E P F R P P P I T P H E Y M L S L Y R T L S D A D R K G G N S S V 192
 AATGTCAGG CTGACCTTGG CAACACCATC ACCAGCTTTA TTGACAAAG GCAAGTAC CGAGGTCCG TGGTACGAA GCAGAGTAC GTGTTTCA CA TTACTGCCCT GGAGAAGGAT
 K L E A G L A N T I T S F I D K G Q D D R G P V V R K Q R Y V F D I S A L E K D 232
 GGGCTGCTG GGGCCGAGCT CGGATCTTG CGGAGAGC CTTGAGAC GGGTCCCC CGAGCGGG GGTGCCAG CTGAAGCTGT CCAGCTGCC CAGCGGCCG
 G L G A E L R I L R K K P S D T A K P A V P R S R R A A Q L K L S S C P S G R 272
 CAGCGCGCG CCTTCTGGA TGTGGCTCC GTGCCAGGC TGACGATC TGCTGGAG GTGTTGACA TCTGGAAGCT CTTTGAAC TTTAAGAACT CGGCCAGCT GTGCTGGAG
 Q P A A L L D V R S V P G L D G S G W E V F D I W K L F R N F K N S A Q L C L E 312
 CTGCAACCT GGAACCGG CAGACCGTG GACCTCCGTG GCTGGGCTT CGACCGGCTT TCCACGAGAA GGCCTGTGTC CTGTGTTTG GCGCACCAA GAAACGGAC
 L E A W E R G R T V D L R G L G F D R A A R Q V H E K A L F L V F G R T K K R D 352
 CTGTTCTTTA ATGAGATTAA GGGCGCTCT GGGCAGAG ATAGACGCT GTATGAGTAC CTGTTGAGC AGCGGGGAA AGCGGGGCTT CCATCGGCA CTTGCCAGGG CAAGGACCC
 L F F N E I K A R S G Q D D K T V Y E Y L F S Q R R K R R A P S A T R Q G K R P 392
 AGCAAGACC TTAAGGCTG CTGCACTGG AAGGCACTC ATGTCAACTT CAAGCACATG GCTTGGAG GCTTGGAGT CCGACCCCTT GAGTACGAG CTTTCCACTG CGAGGGGCTG
 S K N L K A R C S R K A L H V N F K D M G W D D W I L A P L E Y E A F H C E G L 412
 TGGAGTTCC CATTCGCTC CACCTGGAG CCACGAATC ATGAGTCTT CCAGACCTG ATGACTGCA TGGACCCCGA GTCCACCCA CCACCTGCT GTGTGCCCA CCGGCTGAGT
 C E F P L R S H L E P T N H A V I O T L M N S M D P E S T P P T C C V P T R L S 472
 CCATCAGCA TCTCTTCTT TCACTCTGC AACACGTTG TGTATGCA GTATGAGGAC ATGCTGCTG AGTCGTGAG CAGCAGCTAG CAGCAGCTG CTTCTGCTT CTTGCTGCTG 501
 P I S I L F I D S A N N V V Y K Q Y E D M V V E S C G C R . (SEQ. ID NO.: 13)
 ACATCCCAAG AGCCCTTCC TCACTCTG GAATCAGCA GGGTACAGA AGCTTGGCA GAGCATCTA CACAGCTTG TGAAGGATT CAATAGCTT GCTGCTCTC TGAGTGTGAC
 TTGGCTTAA GGGCCCTTT TATCACAAG TTCCCTTGG TGAGATTGC TGCCGCTGCTG CTGATGTGAC CAGTGGAGG CACAGTCCA GGGAGACAGA CTCTGAATGG GACTGAGTCC
 CAGAAACAG TGTCTTCCGA TGAGACTTCAG CCACCATTT CAGCTCTGCA AGCTCTGGA CTCTCTAAG CACCTCTCAG GAGAGCACA GTGCCACTG CTTCTCTCAA
 TCACTTTGT GCTGCTGAC TTCTGTGCC TGGACAGTT GAGAGCTGA CTGGCAAGA AGAGGAGAG AGTTGAGTAG AGTTGAGTAG TGTGAGGCTG TTGACTGTT
 AGATTAAAT GTATTATGAT GAGATAAAA GCAAACTGT GCCTAAAAA AAAAAAAAA A (SEQ. ID NO.: 11)

FIGURE 1

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CGAGCTCG CCGAGCTGG GTCCGCGAG GGAATGCGA CCGCGGCGC AGGAGGATG CCGCGGCGC CGAGAGAGA TCCACGGCC CGGAGCGCC TCGATCGCA GGAGCCCGC 120
 R A S A E L G S A K G H R T R K E G R H P R A P R E N A T A R E P L D R Q E P P
 CCGAGCGCC AGAGGAGCC CCGCGGCGC CCGCGGCGC AGCTGAGC TCGGAGCCT CCGCGGCGC GAGTACATGC TGTCAATCTA CAGGACTTAC 240
 P R P Q E F P Q R R P P Q Q P E A R E P P G R G P R L V P H E Y H L S I Y R T Y
 TCGATCGCC AGAGCTGGG CATCAATGCT AGCTTTTCC AGCTTTTCC AGCTTTTCC GTCCGCTAAT AGCTTTTCC GTCTTTTCC GTCTTTTCC GTCTTTTCC GTCTTTTCC 360
 S I A E K L G I N A S F F Q S S K S A N T I T S F V D R G L D D L S H T P L R R
 CAGAATAT TGTTCATGT GTCCAGCTC TCAGACAAAG AGAGCTGT GTCCGCGGAG GTCCGCGGAG GTCCGCGGAG GTCCGCGGAG GTCCGCGGAG GTCCGCGGAG 480
 O K Y L F D V S T L S D K E E L V G A D V R L F R Q A P A A L A P A A A P L A
 GTCTTCGCC TCCAGTCC CCGTGTCT GGAAGCGCG AGCTTGACC CCGAGGCGC CCGCGGCGC GTCTGGAAG GTCTGGAAG GTCTGGAAG GTCTGGAAG GTCTGGAAG 600
 A L R L P V A P A A G S A E P G P A G A P R P G W E V F D V W R G L R P Q P W K
 CAGCTTCT TCGAGTTCT GCGCGGCGC GCGCGGCGC GCGCGGCGC GCGCGGCGC GCGCGGCGC GCGCGGCGC GCGCGGCGC GCGCGGCGC 720
 Q I C L E L R A A W G G E P G A A E D E A R T P G P Q Q P P P P D L R S L G F G
 CCGAGGCTG CCGAGGCTG TGTCTGCTG TGTCTGCTG TGTCTGCTG TGTCTGCTG TGTCTGCTG TGTCTGCTG TGTCTGCTG TGTCTGCTG 840
 R R V R T P Q E R A L L V V F S R S O R K T L F A E H R E Q L G S A T E V V G P
 GGTGTGTGG CCGAGGCTG GCGCGGCGC CCGCGGCGC CCGCGGCGC CCGCGGCGC CCGCGGCGC CCGCGGCGC CCGCGGCGC CCGCGGCGC 960
 G G A E G S G P P P P P P P P P P P S G T P D A G L W S P S P G R R R T A F A
 AGCTTCACG CCGAGGCGC CCGAGGCGC CCGAGGCGC CCGAGGCGC CCGAGGCGC CCGAGGCGC CCGAGGCGC CCGAGGCGC CCGAGGCGC 1080
 S R H G K R H G K K S R L R C S K K P L H V N F K E L G W D D M L L A P L E Y E
 GCCTACCACT CCGAGGCGC GTCCGCTTC CCGTACCT CCGAGGCGC CCGAGGCGC CCGAGGCGC CCGAGGCGC CCGAGGCGC CCGAGGCGC CCGAGGCGC 1200
 A L H C E S V C D E P L R S H L E P T N H A L L Q T L M N S H D P G S T P P S C
 TCGCTGCCA CCAATTCAC TCCATCAGC ATCTTTTGA TCGAGCGCG CCAATTCAG TCGTACACG AGTACAGGA GATGTGTGT GATGTGTGT GATGTGTGT 1308
 V P T K L T P I S I L Y I D A G N N V V Y N E Y E E M V V E S C G C R

FIGURE 2

3/4

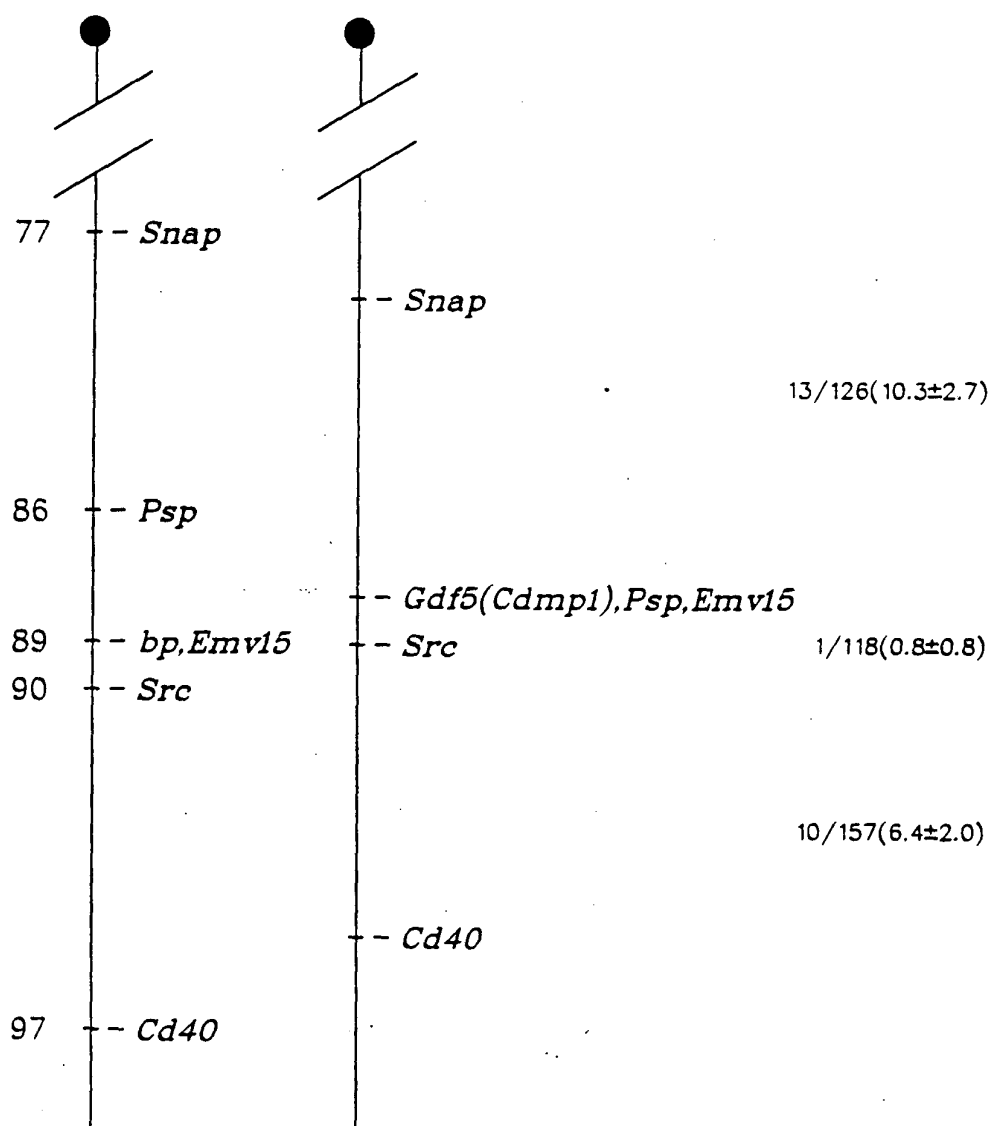


FIG. 3

4 / 4

Xenopus CDMP-x	WI	I	APL	E	YEA	H	HCEG	V	C	D	FP	LRSHLEPTNH	A	(SEQ ID NO:16)
Human CDMP-1	WI	I	APL	E	YEA	F	HCEG	D	C	E	FP	LRSHLEPTNH	A	(SEQ ID NO:17)
Chicken CDMP-x	WI	I	APL	E	YEA	Y	HCEG	D	C	E	FP	LRSHLEPTNH	A	(SEQ ID NO:18)
Zebrafish CDMP-3	WI	V	APL	D	YEA	Y	HCEG	V	C	D	FP	LRSHLEPTNH	A	(SEQ ID NO:19)
Xenopus CDMP-x	WI	I	APL	E	YEA	Y	HCEG	V	C	D	FP	LRSHLEPTNH	A	(SEQ ID NO:20)
Human CDMP-2	WI	I	APL	E	YEA	Y	HCEG	V	C	D	FP	LRSHLEPTNH	A	(SEQ ID NO:21)
Bovine CDMP-2	WI	I	APL	E	YEA	Y	HCEG	V	C	D	FP	LRSHLEPTNH	A	(SEQ ID NO:22)
Zebrafish CDMP-x	WI	M	APL	D	YEA	Y	HCEG	D	C	D	FP	LRSHLEPTNH	A	(SEQ ID NO:23)
Consensus	WI	I	APL	E	YEA	Y	HCEG	V	C	D	FP	LRSHLEPTNH	A	(SEQ ID NO:24)

FIGURE 4

See substitute figures 4 filed 12/11/200 (Ex. 4)
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